

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 8, 2004, 05:41:17 ; Search time 78 Seconds
(without alignments)
1060.098 Million cell updates/sec

Title: US-09-659-379-6_COPY_27_175

Perfect score: 819
Sequence: 1 EBSGKULPSSRITCPQGSVA.....OKMRDPCNENLPYICKRV 149

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09659379/rnat 30072004.175948.21071/app.query.fasta_1.327
-DB=Issued Patents NA -OPMT=fastlap -SUFFIX=tni -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09659379.@cgn 1.1.69 @rnat 30072004.175948.21071 -NCPU=6 -ICPU=3
-NO MMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPO2=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/2/ina/5A COMB.seq: *
2: /cgn2_6/prodata/2/ina/5B COMB.seq: *
3: /cgn2_6/prodata/2/ina/6A COMB.seq: *
4: /cgn2_6/prodata/2/ina/6B COMB.seq: *
5: /cgn2_6/prodata/2/ina/6C COMB.seq: *
6: /cgn2_6/prodata/2/ina/6D COMB.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	819	100.0	558	1	US-08-909-725-4 Sequence 4, Appli
2	819	100.0	586	3	US-09-146-969-3 Sequence 3, Appli
3	819	100.0	747	2	US-08-401-530A-1 Sequence 1, Appli
4	819	100.0	747	2	US-08-709-662-1 Sequence 1, Appli
5	511	62.4	474	1	US-07-778-156-8 Sequence 8, Appli
6	511	62.4	474	2	US-08-422-166-1 Sequence 8, Appli
7	511	62.4	793	1	US-07-778-156-1 Sequence 1, Appli
8	511	62.4	793	2	US-08-422-166-1 Sequence 1, Appli
9	491	60.0	797	2	US-08-464-637-1 Sequence 1, Appli
10	491	60.0	797	2	US-08-822-261-5 Sequence 5, Appli
11	491	60.0	797	4	US-09-226-852-5 Sequence 5, Appli
12	485	59.2	522	1	US-07-778-156-4 Sequence 4, Appli

13	485	59.2	522	2	US-08-422-166-4 Sequence 4, Appli
14	485	59.2	762	2	US-08-822-261-2 Sequence 2, Appli
15	485	59.2	762	4	US-09-226-852-2 Sequence 12, Appli
16	485	59.2	798	1	US-07-778-156-12 Sequence 6, Appli
17	485	59.2	798	2	US-08-822-261-6 Sequence 12, Appli
18	485	59.2	798	2	US-08-422-166-12 Sequence 6, Appli
19	485	59.2	798	4	US-09-146-969-2 Sequence 2, Appli
20	485	59.2	798	3	US-09-146-969-2 Sequence 2, Appli
21	361	44.1	602	3	US-09-385-982-257 Sequence 257, App
22	333.5	40.7	777	3	US-09-146-969-1 Sequence 1, Appli
23	276.5	33.8	590	2	US-08-454-557C-32 Sequence 32, Appli
24	276.5	33.8	590	2	US-08-340-460D-32 Sequence 32, Appli
25	276.5	33.8	590	2	US-08-450-673C-32 Sequence 32, Appli
26	276.5	33.8	590	5	PCT-US95-17111A-32 Sequence 32, Appli
27	249.5	30.5	610	3	US-09-385-982-229 Sequence 229, App
28	198.5	24.2	378	2	US-08-454-557C-16 Sequence 16, Appli
29	198.5	24.2	378	2	US-08-450-673C-16 Sequence 16, Appli
30	198.5	24.2	378	2	US-08-340-460D-16 Sequence 16, Appli
31	198.5	24.2	378	5	PCT-US95-17111A-16 Sequence 16, Appli
32	186.5	22.8	614	2	US-08-729-103-2 Sequence 2, Appli
33	186.5	22.8	1114	2	US-08-468-413-1 Sequence 1, Appli
34	186.5	22.8	1114	3	US-09-162-508-1 Sequence 1, Appli
35	186.5	22.8	1114	5	PCT-US95-07169-1 Sequence 1, Appli
36	173	21.1	544	4	US-09-058-740-1 Sequence 1, Appli
37	166.5	20.3	508	4	US-09-621-976-952 Sequence 952, App
38	161	19.7	5169	4	US-09-194-612A-2 Sequence 2, Appli
39	157	19.2	4588	3	US-08-840-062-1 Sequence 1, Appli
40	156	19.0	4411	3	US-09-146-969-4 Sequence 4, Appli
41	156	19.0	4771	3	US-08-840-062-3 Sequence 3, Appli
42	156	19.0	5633	4	US-09-023-655-1490 Sequence 1490, App
43	151	18.4	622	3	US-09-385-982-224 Sequence 24, App
44	149.5	18.3	690	2	US-08-612-840A-7 Sequence 7, Appli
45	149.5	18.3	5191	1	US-08-340-428B-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-909-725-4
Sequence 4, Application US/08909725
Patent No. 5804421
GENERAL INFORMATION:
APPLICANT: Vinitx, Aaron
APPLICANT: Piltenger, Gary
APPLICANT: Rateloff-Phail, Ronit
APPLICANT: Barlow, Scott
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: INGNP IN BACTERIAL AND EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/909,725
FILING DATE: 12-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/741,096
FILING DATE: 30-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 0570.05173
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: 97430 BMB UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 558 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-909-725-4

Alignment Scores:

Pred. No.:	1.94e-90	Length:	558
Score:	819.00	Matches:	149
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1	Indels:	0
		Gaps:	0

US-09-659-379-6_COPY_27_175 (1-149) x US-08-909-725-4 (1-558)

QY 1 GluGluSerGlnLysLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
DB 12 GAAGATCTCAAAAGAAAGAACTGCTCTTCTCAGTAACTGCTCCTCAAGGCTCTGAGCC 71
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
DB 72 TATGGGCTCTATGCTATCTCACTGATTTGATACACAGACTGCTCTTAATGACAACTA 131
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuSerThrGlyValIleThr 60
DB 132 TCCTGCCAGATGCATTTCTCAGACACCTGGCATTTCTCTAGACTGGTAAATTC 191
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
DB 192 TTCGGTCTCTCCCTTGTGAAGAACAGTTGACGGCTTACATTCATCTGATGAGACTC 251
QY 81 HisAppProSerHisGlyThrLeuProAsnGlySerGlyTyrLysTyrSerSerAsn 100
DB 252 CATGATCCCTCAATGATGACCTACCAACGAGAGTGAAGTGAAGGACAGTTCCAAAT 311
QY 101 ValLeuThrPheTyrAsnTyrGlnLysProSerIleAlaAlaAspArgGlyTyrCys 120
DB 312 GTCGTCACCTTCTATTAACCTGGAGAGAACCCCTCTATGCTGCTGACCTGTTATGT 371
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTyrPArgAspPheAsnCysGluAsnGlu 140
DB 372 GCAAGTTTGTCTCAAAATCAAGTTTTCAGAACTGAGAGATTTTAAATGTGAATAATGAG 431
QY 141 LeuProTyrIleCysLysPheLysVal 149
DB 432 CTTCCTATATCTGCAAAATTCAGAGTC 458

RESULT 2

US-09-146-969-3
Sequence 3, Application US/09146969
Patent No. 6228585
GENERAL INFORMATION:

APPLICANT: Dieckraefe, Brian K.
TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
FILE REFERENCE: 04255.75314
CURRENT APPLICATION NUMBER: US/09/146,969
CURRENT FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 586
TYPE: DNA
ORGANISM: Homo sapiens
US-09-146-969-3

Alignment Scores:

Pred. No.:	2.08e-90	Length:	586
Score:	819.00 <td>Matches:</td> <td>149</td>	Matches:	149
Percent Similarity:	100.00% <td>Conservative:</td> <td>0</td>	Conservative:	0
Best Local Similarity:	100.00% <td>Mismatches:</td> <td>0</td>	Mismatches:	0
Query Match:	3	Indels:	0
		Gaps:	0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-146-969-3 (1-586)

QY 1 GluGluSerGlnLysLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
DB 72 GAAGATCTCAAAAGAAAGAACTGCTCTTCTCAGTAACTGCTCCTCAAGGCTCTGAGCC 131
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
DB 132 TATGGGCTCTATGCTATCTCACTGATTTGATACACAGACTGCTCTTAATGACAACTA 191
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuSerThrGlyValIleThr 60
DB 192 TCCTGCCAGATGCATTTCTCAGACACCTGGCATTTCTTCACTGCTGGAATTCAC 251
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
DB 252 TCCTGCTCTCCCTTGTGAAGAACAGTTGACGGCTTACATTCATCTGATGAGACTC 311
QY 81 HisAppProSerHisGlyThrLeuProAsnGlySerGlyTyrLysTyrSerSerAsn 100
DB 312 CATGATCCCTCAATGATGACCTACCAACGAGAGTGAAGTGAAGGACAGTTCCAAAT 371
QY 101 ValLeuThrPheTyrAsnTyrGlnLysProSerIleAlaAlaAspArgGlyTyrCys 120
DB 372 GTCGTCACCTTCTATTAACCTGGAGAGAACCCCTCTATGCTGCTGACCTGTTATGT 431
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTyrPArgAspPheAsnCysGluAsnGlu 140
DB 432 GCAAGTTTGTCTCAAAATCAAGTTTTCAGAACTGAGAGATTTTAAATGTGAATAATGAG 491
QY 141 LeuProTyrIleCysLysPheLysVal 149
DB 492 CTTCCTATATCTGCAAAATTCAGAGTC 518

RESULT 3

US-08-401-530A-1
Sequence 1, Application US/08401530A
Patent No. 5834590
GENERAL INFORMATION:

APPLICANT: Vainik, Aaron I.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: IN GAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Allegretti
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 00570.48743
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cricetus
FEATURE:
NAME/KEY: CDS
LOCATION: 20..541
US-08-401-530A-1

Alignment Scores:
Pred. No.: 3e-90 Length: 747
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-08-401-530A-1 (1-747)

QY 1 GluGluSerGlnLysLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 95 GAAGAATCTCAAAAGAAACCTGCTTCTCACTATTAACCTCTCTCAAGGCTCTGTAACC 154
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnIleGluLeu 40
Db 155 TATGGGTCTTATTCCTATTCATCTGATTTGATACCAAGACCTGGTCTAATGACAGAACTA 214
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 50
Db 215 TCCGCGCAGATGATCTTCTCGAGACCTGGCATTTCTCTCACTACTGGTGAATTAAC 274
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrPileGlyLeu 80
Db 275 TTGCTGTCTCTCCCTGTGAAGAACGTTTGACGGCTCTACAGTACATCTGATTGACCTC 334
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrPylsTyrSerSerAsn 100
Db 335 CATGATCCCTCAATGTGTACACTACCAAGGAGTGTGAGTGAAGTGAAGCAATTCAT 394
QY 101 ValLeuThrPheTyrAsnTyrGluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 395 GTCTGTGCTCTCTTAACCTGGAGAGAACCCCTCTATTCCTGTGACCGTGTATTGT 454
QY 121 AlValLeuSerGlnLysSerGlyPheGlnLysTyrArgAspPheAsnCysGluAsnGlu 140
Db 455 GCAGTTTGTCTCAAGAAATCAGGTTTTCAGAGTGAAGAGATTTTATTGTGAATAATGAG 514
QY 141 LeuProTyrTyrLeuGlySerPheLeuVal 149
Db 515 CTTCCTATATCTGCAAAATTCAGAGTC 541

RESULT 4

US-08-709-662-1
Sequence 1, Application US/08709662
Patent No. 5840531
GENERAL INFORMATION:
APPLICANT: Vinik, Aaron I.
APPLICANT: Piltenger, Gary L.
APPLICANT: Rafealoff, Ronit
APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INGP PROTEIN INVOLVED IN PANCREATIC

TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: US
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00570.59178
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 747 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Cricetus
FEATURE:
NAME/KEY: CDS
LOCATION: 20..541
US-08-709-662-1

Alignment Scores:

Pred. No.: 3e-90 Length: 747
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-08-709-662-1 (1-747)

QY 1 GluGluSerGlnLysLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 95 GAAGAATCTCAAAAGAAACCTGCTTCTCACTATTAACCTCTCTCAAGGCTCTGTAACC 154
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnIleGluLeu 40
Db 155 TATGGGTCTTATTCCTATTCATCTGATTTGATACCAAGACCTGGTCTAATGACAGAACTA 214
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 60
Db 215 TCCGCGCAGATGATCTTCTCGAGACCTGGCATTTCTCTCACTACTGGTGAATTAAC 274
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrPileGlyLeu 80
Db 275 TTGCTGTCTCTCCCTGTGAAGAACGTTTGACGGCTCTACAGTACATCTGATTGACCTC 334
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrPylsTyrSerSerAsn 100
Db 335 CATGATCCCTCAATGTGTACACTACCAAGGAGTGTGAGTGAAGTGAAGCAATTCAT 394
QY 101 ValLeuThrPheTyrAsnTyrGluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120

Db 395 GTGCTGACCTTCTTAAGTGGAGAGAACCCCTCTATGCTGCTGACCGGTATATGT 454
QY 121 AlAvalleuserglnlySserglyPheglnlystrpArgaspPheasnCygluasnGlu 140
Db 455 GCAGTTTGTCTCGAAGATCAGGTTTTCAGAGTGGAGAGATTTTAATTGGAATAATGAG 514
QY 141 LeuProTyrIleCyGlySPhelysVal 149
Db 515 CTTCCTATATCTGCAAAATCAAGGTC 541

RESULT 5

US-07-778-156-8
; Sequence 8, Application US/07778156
; Patent No. 5436169
; GENERAL INFORMATION:
; APPLICANT: IOVANNA, JUAN-LUCIO
; APPLICANT: KEIM, VOLKER
; APPLICANT: DAGORN, JEAN-CHARLES
; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
; TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
; TITLE OF INVENTION: PANCREATITIS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,156
; FILING DATE: 19911219
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5436169man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 354-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: rat
; TISSUE TYPE: pancreas
; US-07-778-156-8

Alignment Scores:
Pred. No.: 4,166-53 Length: 474
Score: 511.00 Matches: 87
Percent Similarity: 77.70% Conservative: 28
Best Local Similarity: 58.78% Mismatches: 32
Query Match: 62.39% Indels: 1
DB: 1 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) X US-07-778-156-8 (1-474)

QY 1 GluGlnuserglnlySLeuProSerSerArgIleThrCysProGlnlySerValala 20
Db 1 GAAGACTCTCGAAGAAATAACCTCTGACGATTAAGTCCCAAGGCTCCAGGCA 60

QY 21 TyrIglySerTyrCysTyrSerIleuIleuIleProGlnThrTrpSerAsnIleGluLeu 40
Db 61 TATGCTCTCACTGCTATGCGCTCTTTCAGATACACAGACTGTTGATGCGAAGACTG 120
QY 41 SerCysGlnMetHisPheSerSerGlyHisLeuAlaPheLeuLeuSerThrGluIleThr 60
Db 121 GCCTGCCAAGAGAGACTCGAAGGACACCTTATCTGCTGCTCATGTCAGGAGCTTCA 180
QY 61 PheValSerSerLeuValIlyAsnSerIleuThrAlaTyrGlnIlyIleTyrIleGlyLeu 80
Db 181 TTCTTGATCCATGATGTCAGAACACAGCTGAAACAGCTACATATACCTGATGAGCTC 240
QY 81 HisAppProSerHisGlyThrLeuProAsnIlySerGlyTyrIlyStrpSerSerSer 100
Db 241 CATGACCCCTCTCTGCGAGAACCCATGAGCTGATGAGTGAGGAGTGAACATATAC 300
QY 101 ValLeuThrPheTyrAsnTrpGluArgaspProSerIleAlaIleAspArgGlyTyrCys 120
Db 301 ATAATGAATTAATGTCAGACTGCGAGAGAACCATCTATGCTTACACCGGATTTCTGT 360
QY 121 AlAvalleuserglnlySserglyPheglnlystrpArgaspPheasnCygluasnGlu 140
Db 361 GCAGACTTGTCAAGATCTTCTGATTTCTTAAGATGAGAGATACCAATGTAAGTTGA 420
QY 141 -LeuProTyrIleCyGlySPhel 147
Db 421 GTTGCCCTACGCTGCAAAATTT 442

RESULT 6

US-08-422-166-8
; Sequence 8, Application US/08422166
; Patent No. 5959086
; GENERAL INFORMATION:
; APPLICANT: IOVANNA, JUAN-LUCIO
; APPLICANT: KEIM, VOLKER
; APPLICANT: DAGORN, JEAN-CHARLES
; TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
; TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
; TITLE OF INVENTION: PANCREATITIS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,166
; FILING DATE: 14-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/778,156
; FILING DATE: 19-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5959086man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 354-012-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown

TOPOLOGY: unknown
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: pancreas
US-08-422-166-8

Alignment Scores:

Pred. No.:	4,16e-53	Length:	474
Score:	511.00	Matches:	87
Percent Similarity:	77.70%	Conservative:	28
Best Local Similarity:	58.78%	Mismatches:	32
Query Match:	62.39%	Indels:	1
DB:	2	Gaps:	0

US-09-659-379-6_COPY_27_175 (1-149) x US-08-422-166-8 (1-474)

QY 1 GIUGLUSERGlnlylsleuProSerSerArglleThrCysProGlnGlySerValAla 20
Db 1 GAGAGCTCTCCGAAAGAAATATCCCTCTGCAGCATTAAGTGGCCCAAGGCTCCAGGCA 50
QY 21 TYRGLYSERTYrCysTYrSerleuIleuIleProGlnThrTrpSerAsnAlaGluLeu 40
Db 61 TATGCTCTCTACTGCTAGTCCCTGTTTCAATACCAAGACCTGGTTTGAATGCAAGACTG 120
QY 41 SerCysGlnMetHisPheSerGlyHisIleuAlaPheLeuLeuSerThrGlyGluIleThr 50
Db 121 GCGTCCAGAGAGAGACCTGAGAGACACCTTATCTGTGCTCAATGACCTGAAAGCTTCA 180
QY 61 PheValSerSerleuValIysAsnSerleuThrAlaTYrGlnTYrIleTrpIleGlyLeu 30
Db 181 TTCTTGCGATCCAGTGTCAAGAACACCTGAAACAGCTACCAATATACCTGGATTGAGACTC 240
QY 81 HisAspProSerHisGlyThrIleuProAsnGlySerGlyTrpIlySTrpSerSerAsn 100
Db 241 CATGACCCCACTCTGTTGAGAGAACCCAAATGAGAGTGGAGTGGAGTGAACATGAC 300
QY 101 ValLeuThrPheTYrAsnTrpGluArgAsnProSerIleAlaIAspAspGlyTYrCys 120
Db 301 ATATGATATATGTCAACTGGAGAGAGACCAATCTACTCTTAAAGCCCGGATTTCTGT 360
QY 121 AlaValLeuSerGlnIysSerGlyPheGlnIysTrpArgAspPheAsnCysGluAsnGlu 140
Db 361 GGCAGCTGTCAAGATCTTGTGATTTCTAAGATGAGAGATACCAATGTGAAGTTGAA 420
QY 141 -LeuProTYrIleCysIysPhe 147
Db 421 GTTGCCCTACGTCTGCAAAATTT 442

RESULT 7

US-07-778-156-1
Sequence 1, Application US/07778156
Patent No. 5436169
GENERAL INFORMATION:
APPLICANT: IOVANA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/778,156

FILING DATE: 19911219

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, No. 5436169man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 354-012-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)521-4500

TELEFAX: (703)486-2347

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 793 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE:

ORGANISM: rat

TISSUE TYPE: pancreas

FEATURE:

NAME/KEY: CDS

LOCATION: 62..613

US-07-778-156-1

Alignment Scores:

Pred. No.:	9.02e-53	Length:	793
Score:	511.00 <td>Matches:</td> <td>87</td>	Matches:	87
Percent Similarity:	77.70% <td>Conservative:</td> <td>28</td>	Conservative:	28
Best Local Similarity:	58.78% <td>Mismatches:</td> <td>32</td>	Mismatches:	32
Query Match:	62.39% <td>Indels:</td> <td>1</td>	Indels:	1
DB:	1	Gaps:	0

US-09-659-379-6_COPY_27_175 (1-149) x US-07-778-156-1 (1-793)

QY 1 GIUGLUSERGlnlylsleuProSerSerArglleThrCysProGlnGlySerValAla 20
Db 140 GAGAGCTCTCCGAAAGAAATATCCCTCTGCAGCATTAAGTGGCCCAAGGCTCCAGGCA 159
QY 21 TYRGLYSERTYrCysTYrSerleuIleuIleProGlnThrTrpSerAsnAlaGluLeu 40
Db 200 TATGCTCTCTACTGCTAGTCCCTGTTTCAATACCAAGACCTGGTTTGAATGCAAGACTG 259
QY 41 SerCysGlnMetHisPheSerGlyHisIleuAlaPheLeuLeuSerThrGlyGluIleThr 60
Db 260 GCGTCCAGAGAGAGACCTGAGAGACACCTTATCTGTGCTCAATGACCTGAAAGCTTCA 319
QY 61 PheValSerSerleuValIysAsnSerleuThrAlaTYrGlnTYrIleTrpIleGlyLeu 80
Db 320 TTCTTGCGATCCAGTGTCAAGAACACCTTGCAGCATTAAGTGGCCCAAGGCTCCAGGCA 379
QY 81 HisAspProSerHisGlyThrIleuProAsnGlySerGlyTrpIlySTrpSerSerAsn 100
Db 380 CATGACCCCACTCTGTTGAGAGAACCCAAATGAGAGTGGAGTGGAGTGAAGTTGAA 439
QY 101 ValLeuThrPheTYrAsnTrpGluArgAsnProSerIleAlaIAspAspGlyTYrCys 120
Db 440 ATATGATATATGTCAACTGGAGAGAGACCAATCTACTGCTTAAAGCCCGGATTTCTGT 499
QY 121 AlaValLeuSerGlnIysSerGlyPheGlnIysTrpArgAspPheAsnCysGluAsnGlu 140
Db 500 GGCAGCTGTCAAGATCTTGTGATTTCTAAGATGAGAGATACCAATGTGAAGTTGAA 559
QY 141 -LeuProTYrIleCysIysPhe 147
Db 560 GTTGCCCTACGTCTGCAAAATTT 581

RESULT 8

US-08-422-166-1
Sequence 1, Application US/08422166

Patent No. 5959086
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: KEIM, VOLKER
APPLICANT: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
TITLE OF INVENTION: PANCREATITIS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSER: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/422,166
APPLICATION NUMBER: US/08/422,166
FILING DATE: 14-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/778,156
FILING DATE: 19-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5959086man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TEXT: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: cDNA to mRNA
ORIGINAL SOURCE:
ORGANISM: rat
TISSUE TYPE: pancreas
FEATURE:
NAME/KEY: CDS
LOCATION: 62..613
US-08-422-166-1
Alignment Scores:
Pred. No.: 9.02e-53 length: 793
Score: 511.00 Matches: 87
Percent Similarity: 77.70% Conservativity: 28
Best Local Similarity: 58.78% Mismatches: 32
Query Match: 62.39% Indels: 1
DB: 2 Gaps: 0
US-09-659-379-6_COPY_27_175 (1-149) x US-08-422-166-1 (1-793)
QY 1 GluGluSerGlnLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
DB 140 GAAGCTCTCCGAGAAATATACCTCTGACGCAATTAATGTCCTCCCAAGGCTCCGAGCA 199
QY 21 TyrGlySerTyrCysTyrSerIleuLeuIleuProGlnTrpSerAsnAlaGluLeu 40
DB 200 TATGCTCTCTACTGCTATGCTCTGTTTCAGATACCAAGACCTGTTGATGACAGACTG 259
QY 41 SerCysGlnMetHisPheSerGlyHisIleuAlaPheLeuLeuSerThrGlyGlnIleThr 60
DB 260 GCCTGCAGAGAGACCTGAGAGACACTTGTATCTGTGCTCATATGTAGTGAAGCTTCA 319

QY 61 PheValSerSerLeuValLysAsnSerIleuThrAlaTyrGlnIleThrIleTrpIleGlyLeu 80
DB 320 TTTCTGGATTCATGCTCAAGAAACACTGAAACAGCTACCAATATACCTGGATTGACATC 379
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrTrpIleTrpSerSerAsn 100
DB 380 CATGACCCCACTCTTGTGTGAGAACCCAAATGAGGTGGATGGAGATGGAGTAACTATGCT 439
QY 101 ValLeuThrPheTyrAsnTrpGluArgAsnProSerIleAlaAlaAspArgIleTyrCys 120
DB 440 ATATGATATTATCTCAACTGGAGAGAACCACTTACTGCTTACCCCGGATTTCTGT 499
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTrpArgAspPheAsnGlyAsnGlu 140
DB 500 GGCAGCTTGCAAGATCTTCTGATTTCTAAGATGAGAGATACACATGTGAAGTTGA 559
QY 141 -LeuProTyrIleCysLysPhe 147
DB 560 GTTGCCCTACGCTGCAAAATT 581
RESULT 9
US-08-464-637-1
Sequence 1, Application US/08464637
Patent No. 5834214
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCIO
APPLICANT: DAGORN, JEAN-CHARLES
APPLICANT: KEIM, VOLKER
APPLICANT: SARTES, JACQUES
TITLE OF INVENTION: Detection of Pancreatitis-Associated
TITLE OF INVENTION: Protein for Diagnosis of Cystic Fibrosis or Pancreatic
TITLE OF INVENTION: Disease (as amended).
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: USA
ZIP: 22040-3487
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,637
FILING DATE: 30-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 2121-107P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8050
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 43...567
OTHER INFORMATION: /product= "human
OTHER INFORMATION: pancreatitis-associated protein"

ls, Inc.

STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/226,852
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/822,261
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0251 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 262368
US-09-226-852-5

Alignment Scores:
Pred. No.: 2,45e-50 Length: 797
Score: 491.00 Matches: 82
Percent Similarity: 77.55% Conservative: 32
Best Local Similarity: 55.78% Mismatches: 33
Query Match: 59.95% Indels: 0
Gaps: 0
DB:

US-09-659-379-6_COPY_27_175 (1-149) x US-09-226-852-5 (1-797)

QY 1 GluGluSerGlnLysLeuProSerArgIleThrCysProGlnGlySerValAla 20
DB 121 GAAGAACCCCAAGAGGAACTGCTCGAAGATCCGCTGCCAAGGCTCCAGGCC 180
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTrpSerAsnAlaGluLeu 40
DB 181 TATGGCTCCCACTGCTAGTGGCTTTTGTTCACCAAAATCCCGACAGATGACATCTG 240
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuSerThrGlyGluIleThr 60
DB 241 GCCGCCCAAGAGCGCCCTCTGGAACCTGTCTGTCTGCTGAGGGCGTGAAGATCC 300
QY 61 PheValSerSerLeuValIysAsnSerLeuThrAlaTyrGlnTyrIleTrpIleGlyLeu 80
DB 301 TTCTGTCTCTCCCTGGTGAAGCATTTGTGAACACTGATGATGATGGGCTC 360
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrTrpSerSerSerAsn 100
DB 361 CATGACCCCAACAGAGGCGACCGACCATGAGAGGTTGGAGTGGAGTAGAGATGAT 420
QY 101 ValLeuThrPheTyrAsnTrpGluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
DB 421 GTGATGAATTAATCTTTGCAATGGAGAAATCTCTCCACATCTCAAGCCCGGCACTGT 480
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnTyrTrpArgAspPheAsnCysGluAsnGlu 140
DB 481 GCGAGCTGTGAGAGACAGCATTTCTGAGGTGGAAGATTATTAACCTGATATGTGAGG 540

QY 141 LeuProTyrIleCysLysPhe 147
DB 541 TTACCCATGTCTGCAAGTTTC 561

RESULT 12
US-07-778-156-4
Sequence 4, Application US/07778156
Patent No. 5436169
GENERAL INFORMATION:
APPLICANT: IOVANNA, JUAN-LUCCIO
APPLICANT: KEIM, VOLKER
TITLE OF INVENTION: DAGORN, JEAN-CHARLES
TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/778,156
FILING DATE: 19911219
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBION, No. 5436169man F.
REGISTRATION/DOCKET NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 354-012-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)521-4500
TELEFAX: (703)486-2347
TELEX: 248955 OPAT UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULAR TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
TISSUE TYPE: pancreas
US-07-778-156-4

Alignment Scores:
Pred. No.: 6.96e-50 Length: 522
Score: 485.00 Matches: 81
Percent Similarity: 77.40% Conservative: 32
Best Local Similarity: 55.48% Mismatches: 33
Query Match: 59.22% Indels: 0
Gaps: 0
DB:

US-09-659-379-6_COPY_27_175 (1-149) x US-07-778-156-4 (1-522)

QY 1 GluGluSerGlnLysLeuProSerArgIleThrCysProGlnGlySerValAla 20
DB 79 GAAGAACCCCAAGAGGAACTGCTCGAAGATCCGCTGCCAAGGCTCCAGGCC 138
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTrpSerAsnAlaGluLeu 40
DB 139 TATGGCTCCCACTGCTAGTGGCTTTTGTTCACCAAAATCTGAGACAGATGACATCTG 198
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuSerThrGlyGluIleThr 60

Db 199 GCGTGCAGAGGCGCCCTCTGGAACCTGGTGTCTGTCTCAGTGGGGCTGAGGATCC 258
QY 61 PheValSerSerLeuValIysAsnSerLeuThrAlaTyrGlnIleTyrIleGlyLeu 30
Db 259 TTCGTCTCTCTCCCTGGTGAAGACATTGTGAACAGCTACTCATCTCTGGATTGGGCTC 318
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIleTyrSerSerSerAsn 100
Db 319 CATGACCCCAACAGGCGCCAGCCCATGTGAAGAGCTTGGAGTGGAGTACAGTACTGAT 378
QY 101 ValIleuThrPheTyrAsnTyrPgluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 379 GCGATGAATTACTTTCGATGGAAGAAATCCCTCCACCATCTCAAGCCCGGACACTGT 438
QY 121 AlaValIleuSerGlnIysSerGlyPheGlnIysTyrPargAspPheAsnGlyAsnGln 140
Db 439 GCGAGCCTGTGAGAGACACAGCATTTCTGAGGTGAAAGATTATTAAGTATGTGAGG 498
QY 141 LeuProTyrIleCysLys 146
Db 499 TTACCCATGTCTGCATA 516

RESULT 13

US-08-422-166-4

Sequence 4, Application US/08422166

Patent No. 5959086

GENERAL INFORMATION:

APPLICANT: IOVANA, JUAN-LUCIO

APPLICANT: KEIM, VOLKER

APPLICANT: DAGORN, JEAN-CHARLES

TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE

TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 Jefferson Davis Highway, Fourth Floor

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/422,166

FILING DATE: 14-APR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/778,156

FILING DATE: 19-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5959086man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 354-012-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)521-4500

TELEFAX: (703)486-2347

TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 522 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

TISSUE TYPE: pancreas

US-08-422-166-4

Alignment Scores:
Pred. No.: 6,96e-50 Length: 522
Score: 485.00 Matches: 81
Percent Similarity: 77.40% Conservative: 32
Best Local Similarity: 55.48% Mismatches: 33
Query Match: 59.22% Indels: 0
Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-08-422-166-4 (1-522)

QY 1 GlnGluSerGlnIysLeuProSerSerArgIleThrCysProGlnIysValAla 20
Db 79 GAGAAACCCACAGAGGAATGCGCTCTGACGATCCGCTGCCAAGGCTCCAAGGCC 138
QY 21 TyrGlySerTyrCysTyrSerLeuIleuIleProGlnIleTyrSerAsnAlaGluLeu 40
Db 139 TATGGCTCCACTGCTATGCTCTGTGTTTGCACCAAAATCTGACAGATGCAATCTG 198
QY 41 SerCysGlnMetHisPheSerGlyHisPheAlaPheLeuLeuSerThrGlyIleuIleThr 60
Db 199 GCGTGCAGAAAGCGCCCTCTGGAACCTGTGTCTGCTCAGTGGGCTGAGGGATCC 258
QY 61 PheValSerSerLeuValIysAsnSerLeuThrAlaTyrGlnIleTyrIleGlyLeu 80
Db 259 TTCGTCTCTCTCCCTGGTGAAGACATTGTGAACAGTACTCATGCTGTGATTGGGCTC 318
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIleTyrIleTyrSerSerAsn 100
Db 319 CATGACCCCAACAGGCGCCAGCCCAATGGAAGAGTGGAGTGAAGAGATGTGAT 378
QY 101 ValIleuThrPheTyrAsnTyrPgluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 379 GCGATGAATTACTTTCGATGGAAGAAATCCCTCCACCATCTCAAGCCCGGACACTGT 438
QY 121 AlaValIleuSerGlnIysSerGlyPheGlnIysTyrPargAspPheAsnGlyAsnGln 140
Db 439 GCGAGCCTGTGAGAGACACAGCATTTCTGAGGTGAAAGATTATTAAGTATGTGAGG 498
QY 141 LeuProTyrIleCysLys 146
Db 499 TTACCCATGTCTGCATA 516

RESULT 14

US-08-822-261-2

Sequence 2, Application US/08822261

Patent No. 5935813

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: NOVEL HUMAN PANCREATITIS-ASSOCIATED

TITLE OF INVENTION: PROTEIN

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Inocyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/822,261

FILING DATE: Filed Herewith

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

US-08-822-261-2

Mon Aug 9 09:27:51 2004

us-09-659-379-6_copy_27_175.rn1

Page 11

Db 612 TTACCCATGCTGCAAGTTCAAG 635

Search completed: August 8, 2004, 06:58:44
Job time : 82 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Comugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 8, 2004, 06:49:57 ; Search time 412 Seconds

(without alignments)
1773.223 Million cell updates/sec

Title: US-09-659-379-6_COPY_27_175

Perfect score: 819
Sequence: 1 EESQKLPSSRITCPQGSVA.....QKMDPNCENELPYCKRKV 149

Scoring table:

Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Fgapop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 3222919 seqs, 245157024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-O=/cgn2_1/USPTO.spool/US0959379/runat_30072004_175950_21116/app_query.fasta_1.327
-MODEL=frame+ p2n.model -DEV=x1h
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rmpb -MINMATCH=0.1
-TRANSL=0 -LOOEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomsum62
-LDB=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptlo -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptlo -THR SCORE=pct -THR MAX=100
-MAXLEN=200000000 -USER=US0959379@cgn.1.1.519@runat_30072004_175950_21116
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DISPLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA:*

1:	/cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2:	/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3:	/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4:	/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5:	/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6:	/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8:	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9:	/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10:	/cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11:	/cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12:	/cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq:*
13:	/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
14:	/cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16:	/cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17:	/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
------------	-------------	-------	--------	----	-------------

1	819	100.0	525	17	US-10-231-494-18	Sequence 18, Appl
2	819	100.0	586	9	US-09-739-262-3	Sequence 3, Appl
3	819	100.0	747	16	US-10-421-363-2	Sequence 20, Appl
4	799	97.6	445	17	US-10-231-494-20	Sequence 22, Appl
5	791	96.6	441	17	US-10-231-494-22	Sequence 23, Appl
6	582	71.1	6586	16	US-10-339-167-2	Sequence 147, App
7	520	63.5	781	16	US-10-191-803-235	Sequence 146, App
8	517	63.1	528	12	US-09-997-722-147	Sequence 37, Appl
9	517	63.1	759	12	US-09-997-722-146	Sequence 150, App
10	496	60.6	530	16	US-10-028-248A-37	Sequence 149, App
11	491	60.0	528	12	US-10-107-782-37	Sequence 171, App
12	491	60.0	528	12	US-09-997-722-150	Sequence 2, Appl
13	491	60.0	797	15	US-10-316-761-5	Sequence 6, Appl
14	491	60.0	807	12	US-09-997-722-149	Sequence 451, App
15	491	60.0	940	9	US-09-925-301-171	Sequence 451, App
16	485	59.2	762	15	US-10-316-761-2	Sequence 451, App
17	485	59.2	798	9	US-09-739-262-2	Sequence 451, App
18	485	59.2	798	15	US-10-316-761-6	Sequence 451, App
19	485	59.2	859	9	US-09-978-295A-451	Sequence 451, App
20	485	59.2	859	9	US-09-978-697-451	Sequence 451, App
21	485	59.2	859	9	US-09-978-192A-451	Sequence 451, App
22	485	59.2	859	9	US-09-998-832A-451	Sequence 451, App
23	485	59.2	859	10	US-09-978-189-451	Sequence 451, App
24	485	59.2	859	10	US-09-978-608A-451	Sequence 451, App
25	485	59.2	859	10	US-09-978-585A-451	Sequence 451, App
26	485	59.2	859	10	US-09-978-191A-451	Sequence 451, App
27	485	59.2	859	10	US-09-978-403A-451	Sequence 451, App
28	485	59.2	859	10	US-09-978-664A-451	Sequence 451, App
29	485	59.2	859	10	US-09-999-833A-451	Sequence 451, App
30	485	59.2	859	10	US-09-978-824-451	Sequence 451, App
31	485	59.2	859	10	US-09-981-915A-451	Sequence 451, App
32	485	59.2	859	10	US-09-978-585A-451	Sequence 451, App
33	485	59.2	859	10	US-09-978-423A-451	Sequence 451, App
34	485	59.2	859	10	US-09-978-193A-451	Sequence 451, App
35	485	59.2	859	10	US-09-999-830A-451	Sequence 451, App
36	485	59.2	859	10	US-09-978-175A-451	Sequence 451, App
37	485	59.2	859	10	US-09-978-681A-451	Sequence 451, App
38	485	59.2	859	10	US-09-978-643A-451	Sequence 451, App
39	485	59.2	859	10	US-09-978-187B-451	Sequence 451, App
40	485	59.2	859	10	US-09-978-298A-451	Sequence 451, App
41	485	59.2	859	10	US-09-978-188A-451	Sequence 451, App
42	485	59.2	859	10	US-09-978-681A-451	Sequence 451, App
43	485	59.2	859	10	US-09-978-194A-451	Sequence 451, App
44	485	59.2	859	10	US-09-999-829A-451	Sequence 451, App
45	485	59.2	859	10	US-09-978-299A-451	Sequence 451, App

ALIGNMENTS

RESULT 1
US-10-231-494-18
Sequence 18, Application US/10231494
Publication No. US2004002334A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
FILE OF INVENTION: Modified Transferrin Fusion Proteins
TITLE REFERENCE: 54710-5001-US
CURRENT APPLICATION NUMBER: US/10/231,494
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 525
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: INGP
OTHER INFORMATION: sequences

```
FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) ... (525)
US-10-231-494-18

Alignment Scores:
Pred. No.: 4.44e-101 Length: 525
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-231-494-18 (1-525)

QY 1 GUGUGSERGINLYSLYLEUPROSERARGLIETHRCYSPROGINGLYSERVALA 20
DB 79 GAAGATCTCAAAAAATTGGCATCTCTAGAAATTACTTGCACAAAGTTCTGTGCT 138

QY 21 TYRGLYSERTYRCYTYRSEIRLEULEULEIPROGINTHTRPSERASNAIAGLUEN 40
DB 139 TATGGTCTTATGTATTCCTTGAATTTGATTCACAAACTGTGCTATATCTGAATTG 198

QY 41 SERCYGINMETHSPHESERGLYHISLEUALAPHELEUSERTHRGLYGNIETHR 60
DB 199 TCTTGCAATTCATTTTCTGCTCATTTGGCTTTTCTTCTACTGCTGAAATTACT 258

QY 61 PHEVALSERSEIRLEUVALLYSANSEIRLEUTHRALATYRGNIETHR 80
DB 259 TTGTTCTCTCTTGGTTAAAAATCTTGTGACTGCTTACATATATTTGGAATTTGGTTTG 318

QY 81 HISAPPROSERHISGLYTHRLIUPROANGLYSERGLYTRIPLYSTPSEIRSERSEN 100
DB 319 CATGATCCATTCATGACTGTTGCCAAATGTTCTGGTGGAAAGTCTTCTTAT 378

QY 101 VALLEUTHRPHETYSANTTRPGIARGANPROSERILEAALAASPARGLYTYRCYS 120
DB 379 GTTTTACCTTTTATATTTGGAAAGAAATCCATTTATGCTGCTGATGAGGTTATGCT 438

QY 121 ALAVALLEUSERGINLYSERGLYPHEGINLYSTTPARGASPHEANCYSGIUAENGIN 140
DB 439 GCGTGTTCCTCAAAAAATCTGGTTTCAAAAAATGAGAGATTTAATGTGAAAAATGAA 498

QY 141 LEUPROTYRILECYSLYSBHELYSVAL 149
DB 499 TTGCCATATATTTGTAATTTAAAGTT 525

RESULT 2
US-09-739-262-3
; Sequence 3, Application US/09739262
; Patent No. US2002003167A1
; GENERAL INFORMATION:
; APPLICANT: Dieckgraefe, Brian K.
; TITLE OF INVENTION: Gene Markers for Chronic Mucosal Injury
; FILE REFERENCE: 04255,75314
; CURRENT APPLICATION NUMBER: US/09/739,262
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 09/146,969
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 586
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-739-262-3

Alignment Scores:
Pred. No.: 5.22e-101 Length: 586
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
```

```
DB: 9 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-739-262-3 (1-586)

QY 1 GUGUGSERGINLYSLYLEUPROSERARGLIETHRCYSPROGINGLYSERVALA 20
DB 72 GAAGATCTCAAAAAATTGGCATCTCTAGAAATTACTTGCACAAAGTTCTGTGCT 131

QY 21 TYRGLYSERTYRCYTYRSEIRLEULEULEIPROGINTHTRPSERASNAIAGLUEN 40
DB 132 TATGGTCTTATGTATTCCTTGAATTTGATTCACAAACTGTGCTATATCTGAATTG 191

QY 41 SERCYGINMETHSPHESERGLYHISLEUALAPHELEUSERTHRGLYGNIETHR 60
DB 192 TCTGCCAGATGCAATTTCTTCAGACACCTGGCATTTCTTCAGTACTGGGAAATTAC 251

QY 61 PHEVALSERSEIRLEUVALLYSANSEIRLEUTHRALATYRGNIETHR 80
DB 252 TTGTTCTCTCTTGGTTAAAAATCTTGTGACTGCTTACATATATTTGGAATTTGGTTTG 311

QY 81 HISAPPROSERHISGLYTHRLIUPROANGLYSERGLYTRIPLYSTPSEIRSERSEN 100
DB 312 CATGATCCCTCACATGATGACTACCAACGGAAGTGATGGAAGTGAGCAGTTCCAT 371

QY 101 VALLEUTHRPHETYSANTTRPGIARGANPROSERILEAALAASPARGLYTYRCYS 120
DB 372 GTGCTGACCTTCTATATCTGGAGAGAACTCTTATTTGCTGCTGACCGGTATTTGT 431

QY 121 ALAVALLEUSERGINLYSERGLYPHEGINLYSTTPARGASPHEANCYSGIUAENGIN 140
DB 432 GCGTGTTCCTCAAAAAATCTGGTTTCAAAAAATGAGAGATTTAATGTGAAAAATGAG 491

QY 141 LEUPROTYRILECYSLYSBHELYSVAL 149
DB 492 CTTCCCTATATCTGCAAAATTCAGGTC 518

RESULT 3
US-10-421-363-2
; Sequence 2, Application US/10421363
; Publication No. US20040018623A1
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Lawrence
; TITLE OF INVENTION: MEDIUM FOR PREPARING DIFFERENTIATED
; FILE REFERENCE: 701826-05621-CIP
; CURRENT APPLICATION NUMBER: US/10/421,363
; CURRENT FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: US 10/111,485
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: PCT/CA00/01284
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,137
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mammalian INGPAP
; NAME/KEY: CDS
; LOCATION: (20) ... (541)
US-10-421-363-2

Alignment Scores:
Pred. No.: 7.49e-101 Length: 747
Score: 819.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
```

US-09-659-379-6_COPY_27_175 (1-149) x US-10-421-363-2 (1-747)

```
OY 1 GlnGlySerGlnIleuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 95 GAGAAATCTCAAAAGAAAGCTGCTTCTTCACTATTAACCTGCTCAAGGCTCTGTAACC 154
OY 21 TTTGlySerTyrCysTyrSerLeuIleLeuIleProGlnIleThrTyrSerAsnAlaGluLeu 40
Db 155 TATGGGTCTTATTTGCTATTTCACTGATTTTGATACCAAGACCTGGTCTTAATGCAAGACTA 214
OY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyValIleThr 50
Db 215 TCTGGCCAGATGACATTTCTCAAGACACCTGGGATTTCTTCCAGTACCTGGTGAATTTACC 274
OY 61 PheValSerSerLeuValIleAsnSerLeuThrAlaTyrGlnIleTyrIleTyrIleGlyLeu 30
Db 275 TTGGGTCTTCTGCTTGAAGAACGTTTGAAGGCTTCACTGATCATCTGATTTGCACTC 334
OY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrPlysTyrSerSerAsn 100
Db 335 CATATCCCTCACTGACACTGACCTACCCAGAGAGTGGATGGATGGAGAGCAAGTTCCAAAT 394
OY 101 ValLeuThrPheTyrAsnTyrPyluArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 395 GTGCTGACCTTCTTAATCTGGAGAGAGAACCCCTCTATTTGCTGACCTGGTATTATTTGT 454
OY 121 AlaValLeuSerGlnIlePheGlnIleTyrPargAspPheAsnCysGluAsnGlu 140
Db 455 GCAGTTTGTCTCGAAGATCGGTTTTCAGAAAGTGAGAGATTTAATTTGGAAGAAATGAG 514
OY 141 LeuProTyrIleCysLysPheIleVal 149
Db 515 CTTCCCTATATCTGCAATTTCAAGTTC 541
```

RESULT 4

```
US-10-231-494-20
; Sequence 20, Application US/10231494
; Publication No. US20040023334A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 445
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IN GAP
; FEATURE:
; OTHER INFORMATION: sequences for fusion proteins
; NAME/KEY: CDS
; LOCATION: (1)..(444)
US-10-231-494-20
```

Alignment Scores:

```
Pred. No.: 1,79e-98 Length: 445
Score: 799.00 Matches: 144
Percent Similarity: 100.00% Conservative: 2
Best Local Similarity: 98.63% Mismatches: 0
Query Match: 97.56% Indels: 0
DB: 17 Gaps: 0
```

US-09-659-379-6_COPY_27_175 (1-149) x US-10-231-494-20 (1-445)

```
OY 4 GlnIleLysLeuProSerSerArgIleThrCysProGlnGlySerValAlaTyrGlySer 23
Db 4 GAGAAAGCTTCCATCTTCCAGAAATTAATCTGTCACCAAGGTTCTGTTAGTTCT 63
OY 24 TyrCysTyrSerLeuIleLeuIleProGlnIleThrTyrSerAsnAlaGluLeuSerGln 43
Db 64 TATGTTATTTGATTTGATTTTATTCACAAACTGGTCTTAATGCGAATTTGCTGTGCA 123
OY 44 MethiPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyValIleThrPheValSer 63
Db 124 ATGATTTTCTGTCATTTGGCTTTTGTGTTGTTCTACTGATGGAATTAATCTTTGTTCT 183
OY 64 SerLeuValIleAsnSerLeuThrAlaTyrGlnIleTyrIleTyrIleGlyLeuHisAspPro 83
Db 184 TCTTGGTTAAATAATCTTGTACGCTTATCAATATATTTGGATTTGTTGATGATCA 243
OY 84 SerHisGlyThrLeuProAsnGlySerGlyTyrPlysTyrSerSerSerAsnValLeuThr 103
Db 244 TCTATGTTACTTTGCGAATGTTCTGGTTGGAATGGTCTTCTTAATGTTTGAAT 303
OY 104 PheTyrAsnTyrPyluArgAsnProSerIleAlaAlaAspArgGlyTyrCysAlaValLeu 123
Db 304 TTTTACAAATGGGAAAGAAATCCATCTATTTCTGCTGATAGAGTTATTTGCTGTTTG 363
OY 124 SerGlnIleSerGlyPheGlnIleTyrPargAspPheAsnCysGluAsnGluLeuProTyr 143
Db 364 TCTCAAAATCTGTTTCAAAATGAGAGATTTAATTTGTAAGAAATGAAATTTGCCATAT 423
OY 144 IleCysLysPheIleVal 149
Db 424 ATTTGTAAATTTTAAAGTT 441
```

RESULT 5

```
US-10-231-494-22
; Sequence 22, Application US/10231494
; Publication No. US20040023334A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IN GAP
; FEATURE:
; OTHER INFORMATION: sequences for fusion proteins
; NAME/KEY: CDS
; LOCATION: (2)..(436)
US-10-231-494-22
```

Alignment Scores:

```
Pred. No.: 2.15e-97 Length: 441
Score: 791.00 Matches: 143
Percent Similarity: 99.31% Conservative: 1
Best Local Similarity: 98.62% Mismatches: 1
Query Match: 96.58% Indels: 0
DB: 17 Gaps: 0
```

US-09-659-379-6_COPY_27_175 (1-149) x US-10-231-494-22 (1-441)

```
OY 5 IysLysLeuProSerSerArgIleThrCysProGlnGlySerValAlaTyrGlySerTyr 24
Db 2 CGACCTTGCCTCTTCTCCAGAAATTAATCTGTCACCAAGGTTCTGTTGCTTAT 61
```

QY 25 CysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeuSerCysGlnMet 44
DB 62 TGTATTCTTGTGATTGATCCCAAACTGGCTAATGCTGAATGCTTTCGAATG 121
QY 45 HisPheSerGlyHisIleAlaIlePheLeuLeuSerThrGlyGluIleThrPheValSerSer 64
DB 122 CATTTTCTGGTCAATTTGGCTTTTGTGTGCTGCTGCAATTAATCTTTGTTCTTCT 181
QY 65 LeuValIlyAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeuHisAspProSer 84
DB 182 TTGTTAAATAATCTTTGACAGCTGATCATATATTGATGTTGATGATGATGATGATGAT 241
QY 85 HisGlyThrLeuProAsnGlySerGlyTyrIleTyrPheSerSerSerSerSerValLeuThrPhe 104
DB 242 CATGTTACCTTGGCCAAATGTTGCTGTTGGAATGCTTCTTCTAAATGTTTGAATTTT 301
QY 105 TyrAsnTyrGluArgAsnProSerIleAlaIleAspArgGlyTyrCysAlaValLeuSer 124
DB 302 TACAAATGGGAAAGAAATCCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 361
QY 125 GlnIlySerGlyPheGlnIlySerTyrPheAsnGlyPheAsnGlyLeuGluLeuProTyrIle 144
DB 362 CAAAATCTGTTTCAAAATGAGAGATTTTAATGTGAATAATGAATGGCATATATAT 421
QY 145 CysIlyPheIlyVal 149
DB 422 TGTAAATTTAAAGTT 436

RESULT 6

US-10-339-767-2
Sequence 2, Application US/10339767
Publication No. US20030207301A1
GENERAL INFORMATION:
APPLICANT: GMP Endotherapeutics, Inc.
APPLICANT: Taylor-Fishwick, David A
APPLICANT: Vinik, Aaron I
TITLE OF INVENTION: Assay for the Detection of Factors that Modulate the Expression
FILE REFERENCE: 9061X#L5
CURRENT APPLICATION NUMBER: US/10/339,767
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/388,315
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: US 60/361,073
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 60/346,898
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 6586
TYPE: DNA
ORGANISM: Hamster sp.
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(6586)
OTHER INFORMATION: n = A, C, G, or T
US-10-339-767-2

Alignment Scores:

Pred. No.: 2, 62e-67 Length: 6586
Score: 582.00 Matches: 148
Percent Similarity: 30.27% Conservative: 0
Best Local Similarity: 30.27% Mismatches: 1
Query Match: 71.06% Indels: 341
Gaps: 3

US-09-659-379-6_COPY_27_175 (1-149) x US-10-339-767-2 (1-6586)

QY 1 GlnGluSerGlnIlySerLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
DB 4445 GAAGAAATCTCAAAAGAAATGCTTCTTCAAGTATTAACCTGCTCAAGGCTGTGAGCC 4504

QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGlu 39
DB 4505 TATGGTCTCTATTCCTATTCATGATTTGATACACAGACCTGCTAATGACGAAGTG 4564
QY 39 ----- 39
DB 4565 AGTAGACACACACAGATGGGAACAATAGAACAGAACTTCGGGCTCAAGAGTGCTGT 4624
QY 39 ----- 39
DB 4625 TGGATTCATCTCTGTGTTATTTAGCTAGGAGGAACCAATCCCTCACCTACACTCT 4684
QY 40 ----- LeuSerCys 42
DB 4685 ACCACTCCAGTGGGGTTAATATGTTTCCATTTCTGCTTCCAAACAGCTATCTGCTG 4744
QY 43 GlnMetHisPheSerGlyHisIleAlaIlePheLeuLeuSerThrGlyGluIleThrPheVal 62
DB 4745 CAGATGCAATTTCTCAGACACCTGCAATTTCTCTCAGTACTGCTGGAATTAATCTGCTG 4804
QY 63 SerSerLeuValIlyAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeuHisAsp 82
DB 4805 TCCTCCCTTGTGAAGAACAGTTTGAAGGCTTACAGTATCTGGAATGGAATCATGAT 4864
QY 83 ProSerHis 85
DB 4865 CCTTCACATGTGCGATCCTATCTTGTCTGCTTTTCTCTCATATGAGCTTTATTCCTG 4924
QY 85 ----- 85
DB 4925 TGAAGATTCCTGTGACACCCAGAAAGCAAAATGGGCTCATAGATCTCCAAATGCTGGA 4984
QY 85 ----- 85
DB 4985 TGGCATTAGAGAGAGGAAATATCATGCTGATAGATTAAGTTCTGTGAATCTCAGAGTT 5044
QY 85 ----- 85
DB 5045 CAGTTGAAGTCTGTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5104
QY 85 ----- 85
DB 5105 AATTAATCATCATCTTAAGGAGTCTGCAATATACAGTCTAGTAATGCTGAACAAAGAA 5164
QY 85 ----- 85
DB 5165 TCTTTTGTGTTTCTCTTATAGAAATGATTTTGTTCAGTGTGTTCTGAGAAACCTGCA 5224
QY 85 ----- 85
DB 5225 AAAGTACACCAATTTGATTTATTCAGGAACGTAAATCCAGTAATCCCAATTTTCATT 5284
QY 85 ----- 85
DB 5285 CCATAGTTTCTGGGGGTTTGTAAATAGACGTAGATTTCTGGGATAATATACACAGA 5344
QY 85 ----- 85
DB 5345 AGGCTTTTGGCAATGAGTATGACCATACCAAGTTGTAAAGCTAGGACGGACCAAA 5404
QY 86 ----- -GlyTh 87
DB 5405 TGTTCAGTGAAGATCATGTAATCTGTACCAACCAATCTTGTGACATTTACAGGTTAC 5464
QY 87 rleuProAsnGlySerGlyTyrIleTyrPheSerSerSerSerValIleThrPheTyrAsnTyr 107
DB 5465 ACTAACCCAGAGAGTGTAGAGAGTGAAGTGAACAGTTCCAAATGCTGCTGCTTATATACTG 5524
QY 107 pGluArgAsnProSerIleAlaIleAspArgGlyTyrCysAlaValLeuSerGlnIlySse 127
DB 5525 GAGAGAGAACCCCTCTATGCTGCTGACCGGTGTTATTTGACAGTTTGTCTCAGAAATC 5584

Qy 127 r----- 127
Db 5885 -AGTAAAGACAGAGAGAACCACTGTGATTAAACCATCTTCCACATCCAGTATGACA 5643
Qy 127 ----- 127
Db 5644 COTGGCCATGACAGAGTTTGAGACATACAGTGTGAGCGTGTGTTGTCTCTCTC 5793
Qy 127 ----- 127
Db 5704 ATGTTGCTTATANGTCTCTTGCACAGATATTATCATGCAAGAGATGCTTAAGTC 5763
Qy 127 ----- 127
Db 5764 AAGAGACAGACAGTACATCTTTGTTGAGTTCACAGATTCACTGCCCATCTT 5823
Qy 128 ----- 141
Db 5824 TACCTCTATCTCTCTGTGAGTTTTCAGAGTGGAGAGATTATTTGTAAGTACT 5883
Qy 141 uProtyrilleCyslyspheylsval 149
Db 5884 TCCTATATCTGCAAAATTCAGATC 5908

RESULT 7

US-10-191-803-235
; Sequence 235, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 235
; LENGTH: 781
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_053289
US-10-191-803-235

Alignment Scores:

Pred. No.: 2,846-60 Length: 781
Score: 520.00 Matches: 86
Percent Similarity: 78.23% Conservative: 29
Best Local Similarity: 58.50% Mismatches: 32
Query Match: 63.49% Indels: 0
Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-191-803-235 (1-781)

Qy 1 GluGluSerGlnIlyLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 138 GAAGACTCTCCGAAAGAAATACCTCTGACGCAATTAAGTCCCAAGGCTCCAGGCA 197
Qy 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40

Db 198 TATGGCTCTACTGCTATAGCCCTGTTCAGATACCAAGACCTGTGATGACAGAACTG 257
Qy 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyIleLeuThr 60
Db 258 GCTTGCAGAGAGAGACCTGGAACACCTGTATCTGATCTGTCATGATGAGCTTCA 317
Qy 61 PheValSerSerLeuValIysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
Db 318 TTCTTGGCATTCATGCTGACAGAACACTGGAACAGCTTACCAATATCTGATGAGCTC 377
Qy 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIlyStrPheSerSerAsn 100
Db 378 CATGACCCACTCTGTGGTGGAGAACCAATGAGAGTGGATGGAGTGAATACATGAC 437
Qy 101 ValLeuThrPheTyrAsnTyrGlnArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 438 AATATGATTAATATGCACTGGAGAGAACCACTCTGCTTAAGACCGGAGATTCTGT 497
Qy 121 AlaValLeuSerGlnIlySerGlyPheGlnIlyStrPheAspPheAsnCysGlyAsnGly 140
Db 498 GGCAGCTTGTCAAGATCTTCTGAGTTTCTTAAGATGAGAGATACCAATGTAAGTGAAG 557
Qy 141 LeuProTyrIleCysIlysphe 147
Db 558 TTGCCCTACGCTCCAAATTT 578

RESULT 8

US-09-997-722-147
; Sequence 147, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 147
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-997-722-147

Alignment Scores:

Pred. No.: 4,056-60 Length: 528
Score: 517.00 Matches: 86
Percent Similarity: 77.55% Conservative: 28
Best Local Similarity: 58.50% Mismatches: 33
Query Match: 63.13% Indels: 0
Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-997-722-147 (1-528)

Qy 1 GluGluSerGlnIlyLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 79 GAAGACTCTCCGAAAGAAATACCTCTGACGCAATTAAGTCCCAAGGCTCCAGGCT 138
Qy 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
Db 139 TATGGCTCTACTGCTATAGCCCTGTGTTGAGATACCAAGACCTGTGATGACAAACTG 198
Qy 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyIleLeuThr 60
Db 199 GCTTGCAGAGAGAGCTGGAACCACTGATCTGATCTGCTCAATAGGCTCCAGGCTTCA 258
Qy 61 PheValSerSerLeuValIysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80

```
Db 259 TTCTTGCTCCATGAGTGAAGAGAACAGCAACAGCTACCATACACTTGATGGGCTC 318
Qy 81 HtAspProSerHisGlyThrLeuProAsnGlySerGlyTTrpLysTrpSerSerAsn 100
Db 319 CATGACCCCACTCTGGGTGAGAACCCCAATGAGGTGATGGAGAAATGGAGTAACAATGAC 378
Qy 101 ValLeuThPheThyAsnTrpGluArgAsnProSerLleAlaAlaAspArgGlyTrpCys 120
Db 379 GTGATGAATTACTTTAACTTGGAGAGAACCCATCTACTGCTTAAGCCGCTTCTGT 438
Qy 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTrpArgAspPheAsnCysGluAsnGlu 140
Db 439 GGCAGCTTGTCAGACAGCTCTGGATTCTTAATAATGAGAGATATGACATGTAGGTGAAG 498
Qy 141 LeuProTyrLleCysLysPhe 147
Db 499 TTGCCTATGTCTGCAAAATT 519

RESULT 9
US-09-997-722-146
; Sequence 146, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCP
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 146
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-997-722-146

Alignment Scores:
Pred. No.: 6,94e-60 Length: 759
Score: 517.00 Matches: 86
Percent Similarity: 77.55% Conservative: 28
Best Local Similarity: 58.50% Mismatches: 33
Query Match: 63.13% Indels: 0
DB: 12 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-997-722-146 (1-759)
Qy 1 GluGluSerGlnLysLeuProSerSerArgLleThCysProGlnGlySerValAla 20
Db 110 GAAGACTCCCTGAGAGATATACCTCCGACGCGATTAGTGGCCCAAGGCTCCAGGCT 169
Qy 21 TYRGLYSerTyrCysTrpSerLeuLleLeuLleProGlnThrTrpSerAsnAlaGluLeu 40
Db 170 TATGGCTCTCACTGATGCTGCTTGTTCAGATCCACAGACCTGGTTGATGAGAACTG 229
Qy 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyLleLleThr 60
Db 230 GCCTGCAAAAGAGGCTGAGGACACCTGATCTGTGCTCAATAGCGCTGAGGCTTCA 289
Qy 61 PheValSerSerLleValLysAsnSerLleThrAlaTyrGlnTyrLleTrpLleGlyLeu 80
Db 290 TTCTTGTCTCCATGAGTGAAGAGACAGAAACAGCTACCAATACTTGATGGATGGGCTC 349
Qy 81 HtAspProSerHisGlyThrLeuProAsnGlySerGlyTTrpLysTrpSerSerAsn 100
Db 350 CATGACCCCACTCTGGGTGAGAACCCCAATGAGGTGATGGAGTAACAATGAC 409
Qy 101 ValLeuThPheThyAsnTrpGluArgAsnProSerLleAlaAlaAspArgGlyTrpCys 120
Db 499 TTGCCTATGTCTGCAAAATT 519
```

```
Db 410 GTGATGAATTACTTTAACTTGGAGAGAACCCATCTACTGCTTAAGCCGCTTCTGT 469
Qy 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTrpArgAspPheAsnCysGluAsnGlu 140
Db 470 GGCAGCTTGTCAGACAGCTCTGGATTCTTAATAATGAGAGATATGACATGTAGGTGAAG 529
Qy 141 LeuProTyrLleCysLysPhe 147
Db 530 TTGCCTATGTCTGCAAAATT 550

RESULT 10
US-10-028-248A-37
; Sequence 37, Application US/10028248A
; Publication No. US20030235882A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Patturajan, Meera
; APPLICANT: Vernet, Corine
; APPLICANT: Casman, Stacie
; APPLICANT: Malyankar, Uriel
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Gangolli, Esha
; APPLICANT: Miller, Charles
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Smithson, Glenda
; APPLICANT: Zethusen, Bryan
; APPLICANT: Liu, Xiaohong
; APPLICANT: Colman, Steven
; APPLICANT: Tchernev, Velizar
; APPLICANT: Si, Jingsheng
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Sciore, Paul
; APPLICANT: Millet, Isabelle
; APPLICANT: Rothenberg, Mark
; TITLE OF INVENTION: NO. US0030235882A1el Nucleic Acids and Polypeptides and Methods
; FILE REFERENCE: 21402-222
; CURRENT APPLICATION NUMBER: US/10/028,248A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272408
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/285189
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: 60/308039
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/311266
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 530
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-028-248A-37

Alignment Scores:
Pred. No.: 2,87e-57 Length: 530
Score: 496.00 Matches: 83
Percent Similarity: 77.70% Conservative: 32
Best Local Similarity: 56.08% Mismatches: 33
Query Match: 60.56% Indels: 0
DB: 16 Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-028-248A-37 (1-530)
```

```
QY 1 GluGlnSerGlnValLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 69 GAAAGAACCCCAAGAGGAACTGCTCTGACGAGATCCCTGCCAAAGGCTCCAAAGGCC 128
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
Db 129 TATGCTCCCACTGCTATGCGCTGTGTTTGTTCACCAAAATCTGACAGATGAGATCTG 188
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 50
Db 189 GCGTCCCAAGAGCGGCGCTCTGGAACCTGGTGTCTGTGCTCAGTGCGGCTGAGGAGATCC 248
QY PheValSerSerLeuValLeuAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 30
Db 249 TTCTGTCTCTCCCTGCTGTAAGAGATGTAACAGCTACTCATAGCTGTGATGGGCTC 308
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIleTyrIleSerSerAsn 100
Db 309 CATGACCCCAACAGGAGCGACCGACCCCAATGAGAGAGTTGGAGCTGAGTAGCAATGAT 368
QY 101 ValLeuThrPheTyrAsnTyrGlnArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 369 GTGATGATTAATCTTGTGATGGAGGAATCCCTCCACCATCTCAAGCCCGGCGCACTGT 428
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTyrPheAspPheAsnGlyGluAsnGlu 140
Db 429 GCGAGCCTGTGAGAGACAGCAATTTCTGAGTGGAAGATTAATCAATGATGTGAGG 488
QY 141 LeuProTyrIleCysLysPheLys 148
Db 489 TTACCTATGCTGCAAGTTCAAA 512
RESULT 11
US-10-107-782-37
; Sequence 37, Application US/10107782
; Publication No. US20040018970A1
; GENERAL INFORMATION:
; APPLICANT: Boldog, Ferenc,
; APPLICANT: Caeman, Stacie
; APPLICANT: Colman, Steve,
; APPLICANT: Edinger, Shlomit,
; APPLICANT: Gangolli, Esna,
; APPLICANT: Kekuda, Ramesh,
; APPLICANT: Li, Li,
; APPLICANT: Liu, Xiaohong,
; APPLICANT: Malyanakar, Uriel,
; APPLICANT: Miller, Charles,
; APPLICANT: Miller, Isabelle,
; APPLICANT: Patturajan, Meera,
; APPLICANT: Rothenberg, Mark,
; APPLICANT: Sciore, Paul,
; APPLICANT: Shenoy, Suresh,
; APPLICANT: Shinkets, Richard,
; APPLICANT: Si, Jingsheng,
; APPLICANT: Smithson, Glenda,
; APPLICANT: Spytek, Kimberly,
; APPLICANT: Stone, David,
; APPLICANT: Tchaplev, Raymond, Jr.,
; APPLICANT: Tchernev, Velizar,
; APPLICANT: Vernet, Corine,
; APPLICANT: Zerhusen, Brian
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: 21402-222CIP
; CURRENT APPLICATION NUMBER: US/10107,782
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: 10/028,248
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,619
; PRIOR FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: 60/262,959
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/272,408
```

```
;; PRIOR FILING DATE: 2001-02-28
;; PRIOR APPLICATION NUMBER: 60/285,189
;; PRIOR FILING DATE: 2001-04-20
;; PRIOR APPLICATION NUMBER: 60/308,039
;; PRIOR FILING DATE: 2001-07-26
;; PRIOR APPLICATION NUMBER: 60/311,266
;; PRIOR FILING DATE: 2001-08-09
;; PRIOR APPLICATION NUMBER: 60/279,344
;; PRIOR FILING DATE: 2001-03-28
;; NUMBER OF SEQ ID NOS: 215
;; SOFTWARE: CurSeqdist version 0.1
;; SEQ ID NO 37
;; LENGTH: 530
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (3)..(527)
US-10-107-782-37
Alignment Scores:
Pred. No.: 2,87e-57 Length: 530
Score: 496.00 Matches: 83
Percent Similarity: 77.70% Conservative: 32
Best Local Similarity: 56.08% Mismatches: 33
Query Match: 60.56% Indels: 0
Gaps: 0
US-09-659-379-6_COPY_27_175 (1-149) x US-10-107-782-37 (1-530)
QY 1 GluGlnSerGlnLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
Db 69 GAAAGAACCCCAAGAGGAACTGCTCTGACGAGATCCCTGCCAAAGGCTCCAAAGGCC 128
QY 21 TyrGlySerTyrCysTyrSerLeuIleLeuIleProGlnThrTyrSerAsnAlaGluLeu 40
Db 129 TATGCTCCCACTGCTATGCGCTGTGTTTGTTCACCAAAATCTGACAGATGAGATCTG 188
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGluIleThr 60
Db 189 GCGTCCCAAGAGCGGCGCTCTGGAACCTGGTGTCTGTGCTCAGTGCGGCTGAGGAGATCC 248
QY 61 PheValSerSerLeuValLeuAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
Db 249 TTCTGTCTCTCCCTGCTGTAAGAGATGTAACAGCTACTCATAGCTGTGATGGGCTC 308
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrIleTyrIleSerSerAsn 100
Db 309 CATGACCCCAACAGGAGCGACCGACCCCAATGAGAGAGTTGGAGCTGAGTAGCAATGAT 368
QY 101 ValLeuThrPheTyrAsnTyrGlnArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
Db 369 GTGATGATTAATCTTGTGATGGAGGAATCCCTCCACCATCTCAAGCCCGGCGCACTGT 428
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTyrPheAspPheAsnGlyGluAsnGlu 140
Db 429 GCGAGCCTGTGAGAGACAGCAATTTCTGAGTGGAAGATTAATCAATGATGTGAGG 488
QY 141 LeuProTyrIleCysLysPheLys 148
Db 489 TTACCTATGCTGCAAGTTCAAA 512
RESULT 12
US-09-997-722-150
; Sequence 150, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; CURRENT FILING DATE: 2001-11-30
```

```

; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 150
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-997-722-150

Alignment Scores:
Pred. No.: 1,366-56 Length: 528
Score: 491.00 Matches: 82
Percent Similarity: 77.55% Conservative: 32
Best Local Similarity: 55.78% Mismatches: 33
Query Match: 59.95% Indels: 0
DB: Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-997-722-150 (1-528)

QY 1 GIUGLUSERGILNLYSLYSEUPROSESERARGLIETHRCYSPROGLNGLYSERVALALA 20
DB 79 GAAGAACCCCAAGAGGAACTGCCCTCTGACAGCATCCGCTGCCAAAGCTCCAAAGGCC 138
QY 21 TYRGLYSERTYRCYTSERLEULEULEIPEPROGINTHRTYPSERASNAIAGLUEN 40
DB 139 TATGCTCCACTGCTATGCTGTTTGTTCACCAAAATCTGCAGACATCCAGATCTG 198
QY 41 SERCYGLIMECHISPHESEGLYHISLEUALAPHELEUSEXTHRGYLUILETHR 60
DB 199 GCCTGCCAGAACGGCCCTCTGAAACCTGTGCTGCTCAGTGGGCTCAGGGATCC 258
QY 61 PHEVALSERSEULEVALYLSANSEULEUTHRALATYRGLNLYTTPLEIETPLLEGYLEU 80
DB 259 TTCGTCTCTCCCTGGTGAAGACATTGGTAAACGCTACTCATACCTCTGGAATTGGGCTC 318
QY 81 HISAPPROSEHISGLYTHIRLEUPROAENGLYSERGLYTPLYSTPSESESERASN 100
DB 319 CATGACCCCAACAGAGGACCCCAATGAGAGAGTTGGAGTGGAGTACAGTGTAT 378
QY 101 VALLEUTHRPHETYSANTTPGUAARGANPROSEERLEALALAASPARGLYTYRYS 120
DB 379 GCGATGAATTAATCTTGTCATGAGAGAAATCCCTCCACCATCTCAAGCCCGGCACTGT 438
QY 121 ALAVALLEUSERGLNLYSSEGLYPHEGLNLYSTTPARGASPHSEANCYSGIUAENGLU 140
DB 439 GCGAGCTGTGCGAAGACACAGCATTTCTGAGGTGGAAGATTATTAACGTATATGTGAGG 498
QY 141 LEUPROTYRILECYSLYSPHE 147
DB 499 TTACCTATGTCTGCAAGTTC 519

RESULT 13
US-10-316-761-5
; Sequence 5, Application US/10316761
; Publication NO. US20030109004A1
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; GOLL, SURYA K.
; TITLE OF INVENTION: NOVEL HUMAN PANCAEATITIS-ASSOCIATED
; PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
```

```

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/316,761
; FILING DATE: 10-Dec-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/822,261
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy U.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0251 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 262368
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-316-761-5

Alignment Scores:
Pred. No.: 2,516-56 Length: 797
Score: 491.00 Matches: 82
Percent Similarity: 77.55% Conservative: 32
Best Local Similarity: 55.78% Mismatches: 33
Query Match: 59.95% Indels: 0
DB: Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-10-316-761-5 (1-797)

QY 1 GIUGLUSERGILNLYSLYSEUPROSESERARGLIETHRCYSPROGLNGLYSERVALALA 20
DB 121 GAAGAACCCCAAGAGGAACTGCCCTCTGACAGCATCCGCTGCCAAAGCTCCAAAGGCC 180
QY 21 TYRGLYSERTYRCYTSERLEULEULEIPEPROGINTHRTYPSERASNAIAGLUEN 40
DB 181 TATGCTCCACTGCTATGCTGTTTGTTCACCAAAATCTGCAGACATCCAGATCTG 240
QY 41 SERCYGLIMECHISPHESEGLYHISLEUALAPHELEUSEXTHRGYLUILETHR 60
DB 241 GCCTGCCAGAACGGCCCTCTGAAACCTGTGCTGCTCAGTGGGCTCAGGGATCC 300
QY 61 PHEVALSERSEULEVALYLSANSEULEUTHRALATYRGLNLYTTPLEIETPLLEGYLEU 80
DB 301 TTCGTCTCTCCCTGGTGAAGACATTGGTAAACGCTACTCATACCTCTGGAATTGGGCTC 360
QY 81 HISAPPROSEHISGLYTHIRLEUPROAENGLYSERGLYTPLYSTPSESESERASN 100
DB 361 CATGACCCCAACAGAGGACCCCAATGAGAGAGTTGGAGTGGAGTACAGTGTAT 420
QY 101 VALLEUTHRPHETYSANTTPGUAARGANPROSEERLEALALAASPARGLYTYRYS 120
DB 421 GCGATGAATTAATCTTGTCATGAGAGAAATCCCTCCACCATCTCAAGCCCGGCACTGT 480
QY 121 ALAVALLEUSERGLNLYSSEGLYPHEGLNLYSTTPARGASPHSEANCYSGIUAENGLU 140
DB 481 GCGAGCTGTGCGAAGACACAGCATTTCTGAGGTGGAAGATTATTAACGTATATGTGAGG 540
QY 141 LEUPROTYRILECYSLYSPHE 147
DB 541 TTACCTATGTCTGCAAGTTC 561

RESULT 14
US-09-997-722-149
```

```
; Sequence 149, Application US/09997722
; Publication No. US20040072154A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71171/RMS/DCF
; CURRENT APPLICATION NUMBER: US/09/997,722
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 149
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-997-722-149

Alignment Scores:
Pred. No.: 2,55e-56      Length: 807
Score: 491.00          Matches: 82
Percent Similarity: 77.55%      Conservative: 32
Best Local Similarity: 55.78%      Mismatches: 33
Query Match: 59.95%          Indels: 0
DB: 12                  Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-997-722-149 (1-807)

QY 1 GluGlnSerGlnLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 139 GAAAGAACCCCAAGAGGAACTGCTCTGACGAGATCCGCTCCCAAGGCTCCAAGGCC 198
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 21 TyrGlySerTyrCysTyrSerLeuIleuIleProGlnThrTyrPserAsnAlaGluLeu 40
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 199 TATGGCTCCACCTGATGCTTGTGTTTGTACCAAAATCTTGACGATGCAATGTC 258
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGlnIleThr 50
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 259 GCCTGCCAGAGCGCCCTCTGGAACCTGTGCTGCTCAGTGGGGCTGAGGAGATCC 318
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 319 TTCTGTCTCTCCCTGGTGAGAGATGTAACGACTCATACGCTTGATTTGGGCTC 378
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrPlyTyrPserSerSerAsn 100
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 379 CATGACCCCAACAGGAGGACCGAGCCCAATGAGAGAGTTGGAGTGAAGTACAGTAT 438
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 101 ValLeuThrPheTyrAsnTyrGlnLysArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 439 GTGATGATTTACTTTGATCGATGGAGAGAAATCCCTCCACATCTCAAGCCCGGCACATG 498
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTyrPAspAspPheAsnCysGluAsnGln 140
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 499 GCGAGCCTGTGAGAGAGACAGCATTTCTGAGGTGAGAAAGATTATTAAGTGAATGTGAG 558
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 141 LeuProTyrIleCysLysPhe 147
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 559 TTACCTTANGTCTGCAAGTTTC 579
    |||.....|.....|.....|.....|.....|.....|.....|.....|

RESULT 15
US-09-925-301-171
; Sequence 171, Application US/09925301
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
```

```
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 171
; LENGTH: 940
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (8)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (12)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (919)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (935)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (938)
; OTHER INFORMATION: n equals a,t,g, or c
; OTHER INFORMATION: n equals a,t,g, or c

US-09-925-301-171

Alignment Scores:
Pred. No.: 3.2e-56      Length: 940
Score: 491.00          Matches: 82
Percent Similarity: 77.55%      Conservative: 32
Best Local Similarity: 55.78%      Mismatches: 33
Query Match: 59.95%          Indels: 0
DB: 9                  Gaps: 0

US-09-659-379-6_COPY_27_175 (1-149) x US-09-925-301-171 (1-940)

QY 1 GluGlnSerGlnLysLeuProSerSerArgIleThrCysProGlnGlySerValAla 20
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 156 GAAAGAACCCCAAGAGGAACTGCTCTGACGAGATCCGCTCCCAAGGCTCCAAGGCC 215
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 21 TyrGlySerTyrCysTyrSerLeuIleuIleProGlnThrTyrPserAsnAlaGluLeu 40
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 216 TATGGCTCCACCTGATGCTTGTGTTTGTACCAAAATCTTGACGATGCAATGTC 275
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 41 SerCysGlnMetHisPheSerGlyHisLeuAlaPheLeuLeuSerThrGlyGlnIleThr 60
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 276 GCCTGCCAGAGCGCCCTCTGGAACCTGTGCTGCTCAGTGGGGCTGAGGAGATCC 335
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 61 PheValSerSerLeuValLysAsnSerLeuThrAlaTyrGlnTyrIleTyrIleGlyLeu 80
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 336 TTCTGTCTCTCCCTGGTGAGAGATGTAACGACTCATACGCTTGATTTGGGCTC 395
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 81 HisAspProSerHisGlyThrLeuProAsnGlySerGlyTyrPlyTyrPserSerSerAsn 100
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 396 CATGACCCCAACAGGAGGACCGAGCCCAATGAGAGAGTTGGAGTGAAGTACAGTAT 455
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 101 ValLeuThrPheTyrAsnTyrGlnLysArgAsnProSerIleAlaAlaAspArgGlyTyrCys 120
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 456 GTGATGATTTACTTTGATCGATGGAGAGAAATCCCTCCACATCTCAAGCCCGGCACATG 515
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 121 AlaValLeuSerGlnLysSerGlyPheGlnLysTyrPAspAspPheAsnCysGluAsnGln 140
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 516 GCGAGCCTGTGAGAGAGACAGCATTTCTGAGGTGAGAAAGATTATTAAGTGAATGTGAG 575
    |||.....|.....|.....|.....|.....|.....|.....|.....|
QY 141 LeuProTyrIleCysLysPhe 147
    |||.....|.....|.....|.....|.....|.....|.....|.....|
Db 576 TTACCTTANGTCTGCAAGTTTC 596
    |||.....|.....|.....|.....|.....|.....|.....|.....|

Search completed: August 8, 2004, 08:13:27
Job time : 418 secs
```

